



Figure 1

Sequence Name:

GW.S.ctgl6335-000003.31.0

Figure 1A SEQ ID NO:01

LLAPTGSLFRNCTQDGWSETFPRPNLACGVNVNDSSNEKRSYLLKLKVMYTVGYSSSLVM
LLVALGILCAFRRLHCTRNYIHMHLFVSFILRALSNFIKDAVLFSSDDVTYCDHRGCKL
VMVLFXYCIMANYSWLLVEGSTFTHxLAISFFSERKYLGQFVAFGWGSPAIFVALWAIAR
HFLEDVGCWDINANASIWWIIRGPVILSILNFILFINILRILMRKLRTQETRGNEVSHYK
RLARSTLLLIPLFGIHYIVFAFSPEDAMEIQLFF

Figure 1B SEQ ID NO:02

CTCTTGGCACCCACAGGTTCCCTTGTTCCGAAACTGCACACAGGATGGCTGGTCAGAAACC
TTCCCCAGGCCTAATCTGGCCTGTGGCGTTAATGTGAACGACTCTTCCAACGAGAAGCGG
CACTCCTACCTGCTGAAGCTGAAAGTCATGTACACCGTGGGCTACAGCTCCTCCCTGGTC
ATGCTCCTGGTCGCCCTTGGCATCCTCTGTGCTTTCCGGAGGCTCCACTGCACTCGCAAC
TACATCCACATGCACCTGTTCTGTCCTTCATCCTTCGTGCCCTGTCCAACCTCATCAAG
GACGCCGTGCTCTTCTCCTCAGATGATGTACCTACTGCGATGCCCACAGGGCGGGCTGC
AAGCTGGTCATGGTGCTGTTC

Figure 1C SEQ ID NO:03

TACTGCATCATGGCCAACTACTCCTGGCTGCTGGTGGAAGGCTCTACCTTCACACATNTC
CTCGCCATCTCCTTCTTCTCTGAAAGAAAGTACCTCCAGGGATTTGTGGCATTTCGGATGG
GGTTCTCCAGCCATTTTTGTTGCTTTGTGGGCTATTGCCAGACACTTTCTGGAAGATGTT
GGGTGCTGGGACATCAATGCCAACGCATCCATCTGGTGGATCATTTCGTGGTCCTGTGATC
CTCTCCATCCTGATTAATTTTCATCCTTTTCATAAACATTCTAAGAATCCTGATGAGAAAA
CTTAGAACCCAAGAAACAAGAGGAAATGAAGTCAGCCATTATAAGCGCCTGGCCAGGTCC
ACTCTCCTGCTGATCCCCCTCTTTGGCATCCACTACATCGTCTTCGCCTTCTCCCCAGAG
GACGCTATGGAGATCCAGCTGTTTTTT

Figure 1D SEQ ID NO:04

CTCTTGGCACCCACAGGTTCCCTTGTTCCGAAACTGCACACAGGATGGCTGGTCAGAAACC
TTCCCCAGGCCTAATCTGGCCTGTGGCGTTAATGTGAACGACTCTTCCAACGAGAAGCGG
CACTCCTACCTGCTGAAGCTGAAAGTCATGTACACCGTGGGCTACAGCTCCTCCCTGGTC
ATGCTCCTGGTCGCCCTTGGCATCCTCTGTGCTTTCCGGAGGCTCCACTGCACTCGCAAC
TACATCCACATGCACCTGTTCTGTCCTTCATCCTTCGTGCCCTGTCCAACCTCATCAAG
GACGCCGTGCTCTTCTCCTCAGATGATGTACCTACTGCGATGCCCACAGGGCGGGCTGC
AAGCTGGTCATGGTGCTGTTC
TACTGCATCATGGCCAACTACTCCTGGCTGCTGGTGGAAGGCTCTACCTTCACACATNTC
CTCGCCATCTCCTTCTTCTCTGAAAGAAAGTACCTCCAGGGATTTGTGGCATTTCGGATGG
GGTTCTCCAGCCATTTTTGTTGCTTTGTGGGCTATTGCCAGACACTTTCTGGAAGATGTT
GGGTGCTGGGACATCAATGCCAACGCATCCATCTGGTGGATCATTTCGTGGTCCTGTGATC
CTCTCCATCCTGATTAATTTTCATCCTTTTCATAAACATTCTAAGAATCCTGATGAGAAAA
CTTAGAACCCAAGAAACAAGAGGAAATGAAGTCAGCCATTATAAGCGCCTGGCCAGGTCC
ACTCTCCTGCTGATCCCCCTCTTTGGCATCCACTACATCGTCTTCGCCTTCTCCCCAGAG
GACGCTATGGAGATCCAGCTGTTTTTT



Figure 2

Sequence Name:

GW.S.ctg16490-000000.17.0

Figure 2A SEQ ID NO:05

PTFILFSFQPGDKRTHICVYWEGSEGGHWSTEGCSHVHNSNGSYTKCKCFHLSSFAVLVA
LAPKDPVLTVITQVGLTISLLCLFLAILTFLLCRPIQNTSTSLHLELSLCLFLAHLFLT
GINRTEPELCSIIAGLLHFLYLACFTWMLLEGLHLFLTVRNLKVANYTSTGRFKKRFMYP
VGYGIPAVIIAIVSAIVGPQNYGTFTHCWLKLDKGFIWSFMGPVAVIILNLVFFQVLWIL
RSKLSSLNKEVSTIQDTRVMTFKAISQLFILGCSWGLGFFMVEEVGKTIGSIIAYSFTII
NTLQGVLLFVVHCLLNRRQVR

Figure 2B SEQ ID NO:06

CCCACTTTCATACTATTCTCTTTCCAGCCTGGTGACAAGAGAACAAAACATATCTGTGTC
TACTGGGAGGGATCAGAGGGAGGCCACTGGTCCACGGAGGGCTGCTCTCATGTGCACAGC
AACGGTTCTTACACCAAATGCAAGTGCTTCCATCTGTCCAGCTTTGCCGTCCTCGTGGCT
CTTGCCCCCAAGGAGGACCCTGTGCTGACCGTGATCACCCAGGTGGGGCTGACCATCTCT
CTGCTGTGCCTCTTCCCTGGCCATCCTCACCTTCCCTCCTGTGCCGGCCCATCCAGAACACC
AGCACCTCCCTCCATCTAGAGCTCTCCCTCTGCCTCTTCCCTGGCCCACCTCCTGTTCCCTG
ACGGGCATCAACAGAACTGAGCCTGAGGTGCTGTGCTCCATCATTGCAGGGCTGCTGCAC
TTCCTCTACCTGGCTTGCTTACCTGGATGCTCCTGGAAGGGCTGCACCTCTTCCCTCACC
GTCAGGAACCTCAAGGTGGCCAACTACACCAGCACGGGCAGATTCAAGAAGAGGTTTCATG
TACCCTGTAGGCTACGGGATCCCAGCTGTGATTATTGCTGTGTGTCAGCAATAGTTGGACCC
CAGAATTATGGAACATTTACTCACTGTTGGCTCAAGCTTGATAAAGGATTTCATCTGGAGC
TTCATGGGGCCAGTAGCAGTCATTATCTTGATAAACCTGGTGTTCTACTTCCAAGTTCTG
TGGATTTTGAGAAGCAAACCTTTCCTCCCTCAATAAAGAAGTTTCCACCATTTCAGGACACC
AGAGTCATGACATTTAAAGCCATTTCTCAGCTATTTATCCTGGGCTGTTCTTGGGGCCTT
GGTTTTTTTATGGTTGAAGAAGTAGGGAAGACGATTGGATCAATCATTGCATACTCATTC
ACCATCATCAACACCCTTCAGGGAGTGTTGCTCTTTGTGGTACACTGTCTCCTTAATCGC
CAGGTAAGG



Figure 3

Sequence Name:

GW.S.ctg13100-000000.33.0

Figure 3A SEQ ID NO:07

QHSDAVHDLDDLVDITWVGILLSLVCLLICIFTFCFFRGLQSDRNTIHKNLCSLFFVAELL
FLIGINRTDQPACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESEHSRRKYFYLVG
YGMPALIVAVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATLIIMNVIFLGIALYKMFH
HTAILKPESGCLDNIKLKINIPKSIYIYMYICMCV

Figure 3B SEQ ID NO:08

CAGCACAGTGATGCGGTCCATGACCTCCTTCTGGATGTGATCACGTGGGTGGAATTTTG
CTGTCCCTTGTTTGTCTCCTGATTTGCATCTTCACATTTTGCTTTTCCGGGGGCTCCAG
AGTGACCGTAACACCATCCACAAGAACCCTCTGCATCAGTCTCTTTGTAGCAGAGCTGCTC
TTCCTGATTGGGATCAACCGAACTGACCAACCAATTGCCTGTGCTGTTTTCGCTGCCCTG
TTACATTTCTTCTTCTGGCTGCCTTCACCTGGATGTTCTGGAGGGGGTGCAGCTTTAT
ATCATGCTGGTGGAGGTTTTTGAGAGTGAACATTCACGTAGGAAATACTTTTATCTGGTC
GGCTATGGGATGCCTGCACTCATTGTGGCTGTGTCAGCTGCAGTAGACTACAGGAGTTAT
GGAACAGATAAAGTATGTTGGCTCCGACTTGACACCTACTTCATTTGGAGTTTTATAGGA
CCAGCAACTTTGATAATTATGCTTAATGTAATCTTCCTTGGGATTGCTTTATATAAAATG
TTTCATCATACTGCTATACTGAAACCTGAATCAGGCTGTCTTGATAACATCAAGTTAAAA
ATTAATATTCCAATTATAAAATCTATTTATATCTATATGTATATATGCATGTGTGTG



Figure 4

Sequence Name:

GW.A.ctg12444-000001.0.2

Figure 4A SEQ ID NO:09

GNVAVAFVYYKSI GPLLSSSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEK
ITFTLSHRKTD RYRSLCAFWNYS PDMNGSWSSEGC ELYSNETH TSCRCNHLTHFAILM
SSGPSIIKDYNILTRITQLGIIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAE
LVFLVGINTNTNKFCSIIAGLLHYFFLA AFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYI
FGYLSPAVVVGFS AALGYRYYGTTKVCWLSTENNFIWSFIGPACLIILVCIYKIVITI QK
SDDH

Figure 4B SEQ ID NO:10

GGCAATGTTGCAGTTGCATTTGTATATTATAAGAGTATTGGTCCTTTGCTTTCATCATCT
GACAACTTCTTATTGAAACCTCAA AATTATGATAATTCTGAAGAGGAGGAAAGAGTCATA
TCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCACATTATATGAACTTGAAAAA
ATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATAGGAGTCTATGTGCATTT
TGGAATTACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACA
TACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTTGCAATTTTG
ATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAA
CTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTACCTTCTGGTTCTTC
AGTGAAATTC AAAGCACCAGGACAACAATTCACAAAAATCTTTGCTGTAGCCTATTTCTT
GCTGAACTTGTTTTCTTGTGGGATCAATACAAATACTAATAAGCTCTTCTGTTCAATC
ATTGCCGGACTGCTACACTACTTCTTTTAGCTGCTTTTGCATGGATGTGCATTGAAGGC
ATACATCTCTATCTCATTGTTGTGGGTGTCATCTACAACAAGGGATTTTGCACAAGAAT
TTTTATATCTTTGGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTTCGGCAGCACTAGGA
TACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACA ACTTTATTGG
AGTTTTATAGGACCAGCATGCCTAATCATTCTTGTATGTATATATAAAATTGTTATTACA
ATTCAAAAAAGTGATGATCAT



Figure 5

Sequence Name:

GW.S.ctg12789-000004.100.0

Figure 5A SEQ ID NO:11

GAWATTGCSVAALYLDSTACFCNHSTSFAILLQIYEVQGPEEESLLRTLSTFVCGVSTFCA
LTTTFLLFLVAGVPKSERTTVHKNLTFSLASAEGFLMTSEWAKANEACVAVTVAMHFLFL
VAFSWMLVEGLLLWRKVAVSMHPPGPMRLYHATGWGVPGIVAVTLAMLPDHYVAPGHC
WLVNHTNAIWAFFVGPVLFVLTVS

Figure 5B SEQ ID NO:12

GGTGCCTGGGCCACACAGGCTGCTCCGTGGCTGCCCTGTACCTGGACTCCACCGCCTGC
TTCTGCAACCACAGCACCAGCTTTGCCATCCTGCTGCAAATCTATGAAGTACAGAGAGGC
CCTGAGGAGGAGTCGCTGCTGAGGACTCTGTCAATTTGTGGGCTGTGGCGTGTCTTCTGC
GCCCTCACCACCACCTTCTTGCTCTTCCCTGGTGGCCGGGGTCCCCAAGTCAGAGCGAACC
ACAGTCCACAAGAACCTCACCTTCTCCCTGGCCTCTGCCGAGGGCTTCCTCATGACCAGC
GAGTGGGCCAAGGCCAATGAGGTGGCATGTGTGGCTGTCACAGTCGCAATGCACTTCCTC
TTTCTGGTGGCATTCTCCTGGATGCTGGTGGAGGGGCTGCTGCTGTGGAGGAAGGTGGTA
GCTGTGAGCATGCACCCGGGCCAGGCATGCGGCTCTACCACGCCACAGGCTGGGGCGTG
CCTGTGGGCATCGTGGCGGTACCCTGGCCATGCTCCCCCATGACTACGTGGCCCCCGGA
CATTGCTGGCTCAATGTGCACACAAATGCCATCTGGGCCTTCGTGGGGCCTGTGCTCTTC
GTGCTGACTGTGAGC



Figure 6

Sequence Name:

GW.A.ctg12776-000000.33.0

Figure 6A SEQ ID NO:13

MKSPRRTTLCLMFIVYSSKAALNWNYESITHPLLHEHEPAGEEALRQKRAVATKSPTAE
EYTVNIEISFENASFLDPIKAYLNSLSFPIHGNNTDQITDILSINVTTVCRPAGNEIWCS
CETGYGWPRERCLHNLICQERDVFLPGHHCSCLKELPPNGPFCLLQEDVTLNMRVRLNVG
FQEDLMNTSSALYRSYKTDLETARKGYGILPGFKGVTVTGFKSGSVVVTYEVKTTPPSLE
LIHKANEQVVQSLNQTYKMDYNSFQAVTINESNFFVTPEIIFEGDTVSLVCEKEVLSSNV
SWRYEEQQLEIQNSSRFSIYTALFNNMTSVSKLTIHNITPGDAGEYVCKLILDI FEYECK
KKIDVMPILQILANEEMKVMCDNNPVS LNCCSQGNVNWSKVEWKQEGKINIPGTPETDIDS
SCSRYTLKADGTQCPGSSGTTVIYTCEFISAYGARGSANIKVTFISVANLTITPDPI SV
SEGQNFSEIKCISDVSNYDEVYWNWSAGIKIYQRFYTRRYLDGAESVLT VKTSTREWNGT
YHCIFRYKNSYSIATKDVIHPLPLKLNIMVDPLEATVSCSGSHHIKCCIEEDGDYKVF
HTGSSSLPAAKEVNKKQVCYKHNFNASSVSWCSKTVDVCCHFTNAANNNSVWSPSMKLNLV
PGENITCQDPVIGVGEPGKVIQKLCRFSNPSSPESPIGGTITYKCVGSQWEEKRND CIS
APINSLQMAKLIKSPSQDEMLPTYLKDLSISIDKAEHEISSSPGSLGAIINILDLLSTV
PTQVNSEMMTVLSTVNVILGKPV LNTWKVLQQQWNTNQS SOLLHSVERFSQALQSGDSPPL
SFSQTNVQMSSMVIKSSHPEYQQRFVFPYFDLWGNVVIDKSYLENLQSDSSIVTMAFPT
LQAILAQDIQENNFAESLVMTTTVSHNTTMPFRISMTFKNNSPSGGETKCVFWNFRLANN
TGGWDSSGCVVEEGDGNVTCICDHLTSFSLMSPDSPDPSSLLGILLDIISYVGVGFSI
LSLAACLVVEAVVWKS VTKNRTSYMRHTCIVNIAASLLVANTWFI VVAIQDNRYILCKT
ACVAATFFIHFFYLSVFFWMLTLGLMLFYRLVFI LHETSRSTQKAI AFCLGYGCPLAISV
ITLGATQPREVYTRKNVCNLN WEDTKALLAFAPALII VVVNITITIVVITKILRPSIGD
KPCKQEKSSLFQISKSIGVLTPLLGLTWGFGLTTFVPGTNLVFHII FAILNVQLFILLF
GCLWDLKQEALLNKFSLSRWSSQHSKTS LGSSTPVFSMSSPISRRFNNLFGKTGTYNVST
PEATSSSLENSSSASSLLN

Figure 6B SEQ ID NO:14

ATGAAATCCCCAAGGAGAACCACCTTTGTGCCTCATGTTTATTGTGATTTATTCTTCCAAA
GCTGCACTGAACCTGGAATTACGAGTCTACTATTATCATCCTTTGAGTCTTCATGAACATGAA
CCAGCTGGTGAAGAGGCACTGAGGCAAAAACGAGCCGTTGCCACAAAAAGTCCTACGGCT
GAAGAATACACTGTTAATATTGAGATCAGTTTTGAAAATGCATCCTTCCTGGATCCTATC
AAAGCCTACTTGAACAGCCTCAGTTTTCCAATTTCATGGGAATAACACTGACCAAATTACC
GACATTTTGAGCATAAATGTGACAACAGTCTGCAGACCTGCTGGAAATGAAATCTGGTG
TCCTGCGAGACAGGTTATGGGTGGCCTCGGGAAAGGTGTCTTCACAATCTCATTGTGCAA
GAGCGTGACGTCTTCCTCCAGGGCACCATTGCAGTTGCCTTAAAGAACTGCCTCCCAAT
GGACCTTTTTGCCTGCTTCAGGAAGATGTTACCCTGAACATGAGAGTCAGACTAAATGTA
GGCTTTCAAGAAGACCTCATGAACACTTCTCCGCCCTCTATAGGTCTACAAGACCGAC
TTGGAAACAGCGTTCCGGAAGGGTTACGGAATTTTACCAGGCTTCAAGGGCGTGACTGTG
ACAGGGTTCAAGTCTGGAAGTGTGGTTGTGACATATGAAGTCAAGACTACACCACCATCA
CTTGAGTTAATACATAAAGCCAATGAACAAGTTGTACAGAGCCTCAATCAGACCTACAAA
ATGGACTACAACCTCTTCAAGCAGTTACTATCAATGAAAGCAATTTCTTTGTACACCA
GAAATCATCTTTGAAGGGGACACAGTCACTGCTGGTGTGTGAAAAGGAAGTTTTGTCTCC
AATGTGTCTTGGCGCTATGAAGAACAGCAGTTGGAAATCCAGAACAGCAGCAGATTCTCG
ATTTACACCGCACTTTTCAACAACATGACTTCGGTGTCCAAGCTCACCATCCACAACATC
ACTCCAGGTGATGCAGGTGAATATGTTTGCAAACCTGATATTAGACATTTTGAATATGAG
TGCAAGAAGAAAATAGATGTTATGCCCATCCAAATTTTGGCAAATGAAGAAATGAAGGTG
ATGTGCGACAACAATCCTGTATCTTTGAACTGCTGCAGTCAGGGTAATGTTAATTGGAGC
AAAGTAGAATGGAAGCAGGAAGGAAAAATAAATATTCCAGGAACCCCTGAGACAGACATA
GATTCTAGCTGCAGCAGATACACCCTCAAGGCTGATGGAACCCAGTGCCCAAGCGGGTCTG

FEB 21 2003

TCTGGAACAACAGTCATCTACACTTGTGAGTTCATCAGTGCCTATGGAGCCAGAGGCAGT
GCAAACATAAAAAGTGACATTTCATCTCTGTGGCCAATCTAACAATAACCCCGGACCCAATT
TCTGTTTCTGAGGGACAAAACCTTTTCTATAAAATGCATCAGTGATGTGAGTAACTATGAT
GAGGTTTATTGGAACACTTCTGCTGGAATTAATAATATACCAAAGATTTTATACACGAGG
AGGTATCTTGATGGAGCAGAATCAGTACTGACAGTCAAGACCTCGACCAGGGAGTGGAAT
GGAACCTATCACTGCATATTTAGATATAAGAATTCATACAGTATTGCAACCAAAGACGTC
ATTGTTACCCCGCTGCCCTCTAAAGCTGAACATCATGGTTGATCCTTTGGAAGCTACTGTT
TCATGCAGTGGTTCCCATCACATCAAGTGCTGCATAGAGGAGGATGGAGACTACAAAGTT
ACTTTCCATACGGGTTCCTCATCCCTTCCTGCTGCAAAAAGAAGTTAACAAAAACAAGTG
TGCTACAAACACAATTTCAATGCAAGCTCAGTTTCCTGGTGTTCAAAACTGTTGATGTG
TGTTGTCACTTTACCAATGCTGCTAATAATTCAGTCTGGAGCCCATCTATGAAGCTGAAT
CTGGTTCCCTGGGGAAAACATCACATGCCAGGATCCCGTAATAGGTGTGCGAGAGCCGGGG
AAAGTCATCCAGAAGCTATGCCGGTTCTCAAACGTTCCAGCAGCCCTGAGAGTCCCAT
GGCGGGACCATCACTTACAAATGTGTAGGCTCCAGTGGGAGGAGAAGAGAAATGACTGC
ATCTCTGCCCCAATAAACCTGTCTGCTCCAGATGGCTAAGGCTTTGATCAAGAGCCCCCTCT
CAGGATGAGATGCTCCCTACATACCTGAAGGATCTTTCTATTAGCATAGACAAAGCGGAA
CATGAAATCAGTCTTCTCCTGGGAGTCTGGGAGCCATTATTAACATCCTTGATCTGCTC
TCAACAGTTCCAACCCAAGTAAATTCAGAAATGATGACGCACGTGCTCTCTACGGTTAAT
GTCATCCTTGGCAAGCCCGTCTTGAACACCTGGAAGGTTTTACAACAGCAATGGACCAAT
CAGAGTTCAAGCTACTACATTAGTGGAAAGATTTTCCAAGCATTACAGTCGGGAGAT
AGCCCTCCTTTGTCCTTCTCCCAAACCTAATGTGCAGATGAGCAGCATGGTAATCAAGTCC
AGCCACCCAGAAACCTATCAACAGAGGTTTGTGTTTCCCATACTTTGACCTCTGGGGCAAT
GTGGTCATTGACAAGAGCTATCTAGAAAACCTTGCAAGTGGATTGCTCTATTGTCACCATG
GCTTTCCCAACTCTCCAAGCCATCCTTGCCAGGATATCCAGGAAAATAACTTTGCAGAG
AGCTTAGTGATGACAACCACTGTGAGCCACAATAACAATATGCCATTACAGATTTCAATG
ACTTTTAAGAACAATAGCCCTTCAGGCGGGCAACGAAGTGTGTCTTCTGGAACCTCAGG
CTTGCCAACAACACAGGGGGGTGGGACAGCAGTGGGTGCTATGTAGAAGAAGGTGATGGG
GACAATGTCACCTGTATCTGTGACCACCTAACATCATTCTCCATCCTCATGTCCCTGAC
TCCCCAGATCCTAGTTCTCTCCTGGGAATACTCCTGGATATTATTTCTTATGTTGGGGTG
GGCTTTTCCATCTTGAGCTTGGCAGCCTGTCTAGTTGTGGAAGCTGTGGTGTGGAAATCG
GTGACCAAGAACCGGACTTCTTATATGCGCCACACCTGCATAGTGAATATCGCTGCCTCC
CTTCTGGTCGCCAACACCTGGTTTATTGTGGTCGCTGCCATCCAGGACAATCGCTACATA
CTCTGCAAGACAGCCTGTGTGGCTGCCACCTTCTTCATCCACTTCTTCTACCTCAGCGTC
TTCTTCTGGATGCTGACACTGGGCCTCATGCTGTTCTATCGCCTGGTTTTCTATTCTGCAT
GAAACAAGCAGGTCCACTCAGAAAGCCATTGCCTTCTGTCTTGGCTATGGCTGCCCCACTT
GCCATCTCGGTTCATCACGCTGGGAGCCACCCAGCCCCGGGAAGTCTATACGAGGAAGAAT
GTCTGTTGGCTCAACTGGGAGGACACCAAGGCCCTGCTGGCTTTCGCCATCCCAGCACTG
ATCATTGTGGTGGTGAACATAACCATCACTATTGTGGTCATCACCAGATCCTGAGGCCT
TCCATTGGAGACAAGCCATGCAAGCAGGAGAAGAGCAGCCTGTTTCAGATCAGCAAGAGC
ATTGGGGTCTCACACCACTCTTGGGCCTCACTTGGGGTTTTGGTCTCACCCTGTGTTT
CCAGGGACCAACCTTGTGTTCCATATCATATTTGCCATCCTCAATGTCTTCCAGGGATTA
TTTCATTTTACTCTTTGGATGCCTCTGGGATCTGAAGGTACAGGAAGCTTTGCTGAATAAG
CCTGTGTTTTCTATGAGTTCTCCAATATCAAGGAGATTTAACAATTTGTTTGGTAAAACA
GGAACGTATAATGTTTCCACCCAGAAGCAACCAGCTCATCCCTGGAAAACCTCATCCAGT
GCTTCTTCGTTGCTCAAC



Figure 7

Sequence Name:

GW.S.ctg12776-000000.175.0

Figure 7A SEQ ID NO:15

ILNSKSISNWTFI RDRNSSYILLHSVNSFARRLFIDNIPVDISDVFIHTMGTTISGDNIG
KNFTFSMRINDTSNEVTGRVLISRDELRKVPSPSQVISIAFPTIGAILEASLLENVTVNG
LVLSAILPKELKRISLIFEKISKSEERRTQCVGWHSVENRWDQQACKMIQENSQQAVCKC
RPSKLFTSFSILMSPHILESILTYITYVGLGISICSLILCLSIEVLVWSQVTKTEITYL
RHVCIVNIAATLLMADVWFIVASFLSGPITHHKGCVAATFFVHFFYLSVFFWMLAKALLI
LYGIMIVFHTLPKSVLVAFLSVGYGCPLAIAAITVAATEPGKGYLRPEICWLNWDMTKA
LLAFVIPALAIVVVNLITVTLVIVKTQRAAIGNSMFQEVRAIVRISKNIAILTPLLGLTW
GFGVATVIDDRSLAFHII FSLNFAQFFILVFGTILDPKV

Figure 7B SEQ ID NO:16

ATTCTTAACAGCAAAGCATCTCCAAGTGGACTTTTCATTTCGTGACAGAAACAGCAGCTAT
ATCCTGCTACATTCACTCACTCCTTTGCAAGAAGGCTATTCATAGATAACATCCCTGTT
GACATATCAGATGTCTTCATTCACTATGAGGACCACCATATCTGGAGATAACATTGGA
AAAAATTTCACTTTTTCTATGAGAATTAATGACACCAGCAATGAAGTCACTGGGAGAGTG
TTGATCAGCAGAGATGAAGTTCGGAAGGTGCCTTCCCCTTCTCAGGTCATCAGCATTGCA
TTTCCAAGTATTGGGGCTATTTTGAAGCCAGTCTTTTGGAAAATGTTACTGTAAATGGG
CTTGCTCCTGTCTGCCATTTTGCCCAAGGAAGTAAAAGAATCTCACTGATTTTTGAAAAG
ATCAGCAAGTCAGAGGAGAGGAGGACACAGTGTGTTGGCTGGCACTCTGTGGAGAACAGA
TGGGACCAGCAGGCCTGCAAATGATTCAAGAAAAGTCCCAGCAAGCTGTTTGCAAATGT
AGGCCAAGCAAATTTGTTTACCTCTTTCTCAATTCTTATGTCACCTCACATCTTAGAGAGT
CTGATTCTGACTTACATCACATATGTAGGCCTGGGCATTTCTATTTGCAGCCTGATCCTT
TGCTTGTCATTGAGGTCCTAGTCTGGAGCCAAGTGACAAAGACAGAGATCACCTATTTA
CGCCATGTGTGCATTGTTAACATTGCAGCCACTTTGCTGATGGCAGATGTGTGGTTCATT
GTGGCTTCCTTTCTTAGTGGCCCAATAACACACCACAAGGGATGTGTGGCAGCCACATTT
TTTGTTCAATTTCTTTTACCTTTCTGTATTTTTCTGGATGCTTGCCAAGGCACTCCTTATC
CTCTATGGAATCATGATTGTTTTCCATACCTTGCCCAAGTCAGTCCCTGGTGGCATCTCTG
TTTTTCAGTGGGCTATGGATGCCCTTTGGCCATTGCTGCCATCACTGTTGCTGCCACTGAA
CCTGGCAAAGGCTATCTACGACCTGAGATCTGCTGGCTCAACTGGGACATGACCAAAGCC
CTCCTGGCCTTCGTGATCCCAGCTTTGGCCATCGTGGTAGTAAACCTGATCACAGTCACA
CTGGTGATTGTCAAGACCCAGCGAGCTGCCATTGGCAATTCATGTTCCAGGAAGTGAGA
GCCATTGTGAGAATCAGCAAGAACATCGCCATCCTCACACCACTTCTGGGACTGACCTGG
GGATTTGGAGTAGCCACTGTCTCGATGACAGATCCCTGGCCTTCCACATTATCTTCTCC
CTGCTCAATGCATTCCAGGGTTTCTTCATCCTAGTGTGTTGGAACCATCCTGGATCCAAAG
GTA



Figure 8

Sequence Name:

GW.S.ctg16790-000000.13.0

Figure 8A SEQ ID NO:17

GTTGDWSSEGCSTEVRPEGTVCCCDHLTFFALLLPTLDQSTVHILTRISQAGCGVSMIFL
AFTIILYAFLRLSRERFKSEDAPKIHVALGGSFLNLAFLVNVGSGSKGSDAACWARGA
VFHYFLLCAFTWMGLEAFHLYLLAVRVFNTYFGHYFLKLSLVGWGLPALMVI GTGSANSY
GLYTIRDRENRTSLELCWFREGTTMYALYITVHGYFLITFLFGMVVLALVVKIFTL SRA
TAVKERGKNRKKVLTILGLSSLVGVTWGLAIFTPLGLSTVYIFALFNSLQVDFYILIFY

Figure 8B SEQ ID NO:18

GGGACCACTGGAGACTGGTCTTCTGAGGGCTGCTCCACGGAGGTCAGACCTGAGGGGACC
GTGTGCTGCTGTGACCACCTGACCTTTTTCGCCCTGCTCCTGAGACCCACCTTGGACCAG
TCCACGGTG CATATCCTCACACGCATCTCCAGGCGGGCTGTGGGGTCTCCATGATCTTC
CTGGCCTTACCATTATTCTTTATGCCTTTCTGAGGCTTTCCCGGGAGAGGTTCAAGTCA
GAAGATGCCCCAAAGATCCACGTGGCCCTGGGTGGCAGCCTGTTCTCCTGAATCTGGCC
TTCTTGGTCAATGTGGGGAGTGGCTCAAAGGGGTCTGATGCTGCCTGCTGGGCCCCGGGG
GCTGTCTTCCACTACTTCCTGCTCTGTGCCTTCACCTGGATGGGCCTTGAAGCCTTCCAC
CTCTACCTGCTCGCTGTCAGGGTCTTCAACACCTACTTCGGGCACTACTTCCTGAAGCTG
AGCCTGGTGGGCTGGGGCCTGCCCCCCTGATGGTCATCGGCACTGGGAGTGCCAACAGC
TACGGCCTCTACACCATCCGTGATAGGGAGAACCGCACCTCTCTGGAGCTATGCTGGTTC
CGTGAAGGGACAACCATGTACGCCCTCTATATCACCGTCCACGGCTACTTCCTCATCACC
TTCCTCTTTGGCATGGTGGTCTGGCCCTGGTGGTCTGGAAGATCTTACCCTGTCCCGT
GCTACAGCGGTCAAGGAGCGGGGAAGAACCGGAAGAAGGTGCTCACCCTGCTGGGCCTC
TCGAGCCTGGTGGGTGTGACATGGGGGTGGCCATCTTACCCCGTTGGGCCTCTCCACC
GTCTACATCTTTGCACTTTTCAACTCCTTGCAAGTTGATTTTTACATATTGATCTTCTAT



Figure 9

Sequence Name:

GW.S.ctg12776-000000.172.0

Figure 9A SEQ ID NO:19

NHILDTA AISNWAFIPKNASSDLLQSVNLFARQLHIHNNSENIVNELFIQTKGFHINHN
TSEKSLNFSMSMNNTTEDILGMVQIPRQELRKLWPNASQAISIAFPTLGAILREHLQNV
SLPRQVNLVLSVVLPERLQEIILTFEKINKTRNARAQCVGWHSKKRRWDEKACQMMLDI
RNEVKCRCNYTSVVMFSILMSSKSMDDKVLDYITCIGLSVSISSLVLCIIIEATVWSRV
VVTEISYMRHVCIVNIAVSLLTANVWFIIGSHFNKAQDYNMCAVAVTFFSHFFYLSLFFW
MLFKALLIIYGILVIFRMMKSRMMVIGFAIGYGCPLIIAVTTVAITEPEKGYIRPEACW
LNWDNTKALXAFAPFVIVAVNLIVVLVAVNTQRPSIGSSKSQDVVIMRISKNVAIL
TPLLGLTWGFGIATLIEGTSLTFFHII FALLNAFQFFILLFGTIMDHKV

Figure 9B SEQ ID NO:20

AACCACATCCTCGACACAGCAGCCATTTCAAACCTGGGCTTTTCATTCCCAACAAAAATGCC
AGCTCGGATTTGTTGCAGTCAGTGAATTTGTTTGCCAGACAACTCCACATCCACAATAAT
TCTGAGAACATTGTGAATGAACTCTTCATTGAGACAAAAGGGTTTCACATCAACCATAAT
ACCTCAGAGAAAAGCCTCAATTTCTCCATGAGCATGAACAATACCACAGAAGATATCTTA
GGAATGGTACAGATTCCCAGGCAAGAGCTAAGGAAGCTGTGGCCAAATGCATCCCAAGCC
ATTAGCATAGCTTTCCCAACCTTGGGGGCTATCCTGAGAGAAGCCCACTTGCAAAATGTG
AGTCTTCCAGACAGGTAAATGGTCTGGTGCTATCAGTGGTTTTACCAGAAAGGTTGCAA
GAAATCATACTCACCTTCGAAAAGATCAATAAAACCCGCAATGCCAGAGCCAGTGTGTT
GGCTGGCACTCCAAGAAAAGGAGATGGGATGAGAAAAGCGTGCCAAATGATGTTGGATATC
AGGAACGAAGTGAAATGCCGCTGTAACCTACACCAGTGTGGTGATGTCTTTTCCATTCTC
ATGTCTCCAAATCGATGACCGACAAAGTTCTGGACTACATCACCTGCATTGGGCTCAGC
GTCTCAATCCTAAGCTTGGTTCTTTGCCTGATCATTGAAGCCACAGTGTGGTCCCGGGTG
GTTGTGACGGAGATATCATACATGCGTCACGTGTGCATCGTGAATATAGCAGTGTCCCTT
CTGACTGCCAATGTGTGGTTTATCATAGGCTCTCACTTTAACATTAAGGCCAGGACTAC
AACATGTGTGTTGCAGTGACATTTTTCAGCCACTTTTCTACCTCTCTCTGTTTTTCTGG
ATGCTCTTCAAAGCATTGCTCATCATTTATGGAATATTGGTCATTTTCCGTAGGATGATG
AAGTCCCGAATGATGGTCATTGGCTTTGCCATTGGCTATGGGTGCCATTGATCATTGCT
GTCACTACAGTTGCTATCACAGAGCCAGAGAAAGGCTACATAAGACCTGAGGCCTGTTGG
CTTAACTGGGACAATAACAAAGCCCTTTAAGCATTGTCATCCCGCGTTTCGTATTGTG
GCTGTAAATCTGATTGTGGTTTTGGTTGTTGCTGTCAACACTCAGAGGCCCTCTATTGGC
AGTTCCAAGTCTCAGGATGTGGTCATAATTATGAGGATCAGCAAAAATGTTGCCATCCTC
ACTCCACTGCTGGGACTGACCTGGGGTTTTGGAATAGCCACTCTCATAGAAGGCACTTCC
TTGACGTTCCATATAATTTTTGCCTTGCTCAATGCTTTCCAGGGTTTTTTCATCCTGCTG
TTTGAACCATATGATCACAAGGTA